

OIPE ROUTING SHEET

APPLICATION

IFW DocCode - SEQREQ

Index using Current Date

S/N 10562601

TO BE DELIVERED TO:
Tech Center Scanning

Sequence Rule Compliance Review Item

	CRF, paper copy of sequence listing, and statement that both are same missing
X	CRF contains error(s) according to STIC Report
	CRF damaged or unreadable according to STIC Report
	CRF transferred from prior application is not compliant

Place an “X” in the appropriate box



CHRISTOPHER S. F. LOW
SUPERVISORY PATENT EXAMINER
TECHNOLOGY CENTER 1600

APPLICATION SERIAL NUMBER

S/N 10562601

**DOES NOT COMPLY WITH THE
SEQUENCE RULES. See reasons below.**

The application does not conform to 37 C.F.R. 1.821 – 1.825. See the attached pages.

=====

Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Thu Jun 07 20:19:22 EDT 2007

=====

Reviewer Comments:

<210> 1
<211> 23
<212> DNA
<213> Artificial Sequence
<220>
<223> CodY target sequence

Please explain the source of "<223> CodY target sequence."

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence
<220>
<223> consensus sequence GTP binding motif in CodY homologs
<220>
<221> Xaa
<222> (2)..(2)
<223> Arg
<220>
<221> Xaa
<222> (3)..(3)
<223> Met, Gly, Ile, Lys, Gln
<220>
<221> Xaa
<222> (4)..(4)
<223> Gly
<220>

```
<221> Xaa
<222> (5)..(5)
<223> Thr
<220>
<221> Xaa
<222> (7)..(7)
<223> Ser
<400> 15
Gly Gly Glu Arg Leu Gly Thr Thr
1 5
```

There are no Xaa's at locations 2-4, and 5-7. Why are there Xaa explanations? e.g., "Gly" is at location 2--it can only represent itself; "Glu" is at location 3. Same type of error in Sequence 15.

```
<220>
<221> Variant
<222> (2)..(2)
<223> Ala, Lys
<220>
<221> Variant
<222> (3)..(3)
<223> Phe, Ile
<400> 24
Asp Arg Val Gly
1
```

The <222> and <223> responses above are invalid. "Arg" is at location 2--it can only represent itself. If you want location 2 to represent Arg, Ala, or Lys, please use "Xaa" instead of "Arg." Same problem with the <222> (3)..(3) and the <223> line below it.

Same type of error in Sequence 29.

```
<210> 226
<211> 30
<212> DNA
<213> Artificial Sequence
<220>
<223> MUT16
```

The <223> response above is an insufficient explanation for <213>

Artificial Sequence. Please give the source of "MUT16." Same type of
error throughout the submitted file.

Application No: 10562601 Version No: 10

Input Set:

Output Set:

Started: 2007-06-07 15:32:33.514
Finished: 2007-06-07 15:32:36.262
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 748 ms
Total Warnings: 207
Total Errors: 12
No. of SeqIDs Defined: 234
Actual SeqID Count: 234

Input Set:

Output Set:

Started: 2007-06-07 15:32:33.514
Finished: 2007-06-07 15:32:36.262
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 748 ms
Total Warnings: 207
Total Errors: 12
No. of SeqIDs Defined: 234
Actual SeqID Count: 234

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (39)
W 213	Artificial or Unknown found in <213> in SEQ ID (40)
W 213	Artificial or Unknown found in <213> in SEQ ID (41) This error has occurred more than 20 times, will not be displayed
E 257	Invalid sequence data feature in <221> in SEQ ID (214)
E 257	Invalid sequence data feature in <221> in SEQ ID (214)
E 257	Invalid sequence data feature in <221> in SEQ ID (214)
E 257	Invalid sequence data feature in <221> in SEQ ID (214)
E 257	Invalid sequence data feature in <221> in SEQ ID (227)
E 257	Invalid sequence data feature in <221> in SEQ ID (228)
E 257	Invalid sequence data feature in <221> in SEQ ID (230)

SEQUENCE LISTING

<110> Hengst den, Christiaan D.
Gajic, Olivera
Kuipers, Oscar P.
Kok, Jan
Sikkema, Jan
Geurts, Johannes M.W.
Nauta, Arjen

<120> Methods and means for regulating gene expression

<130> P63590US00

<140> 10562601
<141> 2007-06-07

<150> US 10/562,601
<151> 2005-12-28

<150> PCT/NL2004/000474
<151> 2004-07-02

<150> EP 03077074.7
<151> 2003-07-02

<160> 234

<170> PatentIn Ver. 3.3

<210> 1
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Cody target sequence

<400> 1
atgttcagaa aattcatgaa cat

23

<210> 2
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> primer sto 14

<400> 2
cttgcctatgg aatcaccccg

19

<210> 3
<211> 28

<212> DNA
<213> Artificial Sequence

<220>
<223> primer opp1

<400> 3
gctctagaca ctcacttgg ttgtttcc

28

<210> 4
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer opp2

<400> 4
aactgcagga aaattcatga acataacc

27

<210> 5
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> primer opp3

<400> 5
aactgcagta aaacaataat aaaaggcag

28

<210> 6
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer opp4

<400> 6
aactgcagga taataaaatt tggactg

27

<210> 7
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer opp14

<400> 7
aactgcagcg taatgttcag aaaattc

27

<210> 8
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer opp15 (a)

<400> 8
aactgcagcg taatatttag aaaattcatg aacatacc 38

<210> 9
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer opp15 (b)

<400> 9
aactgcagcg tactgtgccg aaaattcatg aacatacc 38

<210> 10
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> primer cod280A

<400> 10
gggaattcgg attgtctatc tgcctcg 27

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> primer cod280B

<400> 11
gggggatcca gatctgacca tgattacgcc aagctt 36

<210> 12
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> primer HC-5

<400> 12
ctagaccacc atggggcata accatcacca tcacgtggct acattacttg aaaaaacacg 60

<210> 13
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> primer HC-6

<400> 13
ctagtctaga tttagaaatta cgtccagcaa gtttatac 37

<210> 14
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> inversely repeated (IR) cis-element

<400> 14
aattttcwga aaatt 15

<210> 15
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence GTP binding motif in CodY homologs

<220>
<221> Xaa
<222> (2)..(2)
<223> Arg

<220>
<221> Xaa
<222> (3)..(3)
<223> Met, Gly, Ile, Lys, Gln

<220>
<221> Xaa
<222> (4)..(4)
<223> Gly

<220>
<221> Xaa
<222> (5)..(5)
<223> Thr

<220>
<221> Xaa
<222> (7)..(7)
<223> Ser

<400> 15
Gly Gly Glu Arg Leu Gly Thr Thr
1 5

<210> 16
<211> 8
<212> PRT
<213> Escherichia coli

<220>
<221> BINDING
<222> (1)..(8)
<223> /note="Putative GTP binding motif G1"

<400> 16
Leu Gly Gly Gly Thr Gly Thr Gly
1 5

<210> 17
<211> 8
<212> PRT
<213> Bacillus subtilis

<220>
<221> BINDING
<222> (1)..(8)
<223> /note="Putative GTP binding motif G1"

<400> 17
Gly Gly Glu Arg Leu Gly Thr Leu
1 5

<210> 18
<211> 8
<212> PRT
<213> Bacillus halodurans

<220>
<221> BINDING
<222> (1)..(8)
<223> /note="Putative GTP binding motif G1"

<400> 18
Gly Gly Gln Arg Leu Gly Thr Leu
1 5

<210> 19

<211> 8
<212> PRT
<213> Clostridium difficile

<220>
<221> BINDING
<222> (1)..(8)
<223> /note="Putative GTP binding motif G1"

<400> 19
Gly Gly Met Arg Leu Gly Ser Leu
1 5

<210> .20
<211> 8
<212> PRT
<213> Clostridium acetobutylicum

<220>
<221> BINDING
<222> (1)..(8)
<223> /note="Putative GTP binding motif G1"

<400> 20
Asn Arg Glu Arg Leu Gly Thr Leu
1 5

<210> 21
<211> 8
<212> PRT
<213> Streptococcus pneumoniae

<220>
<221> BINDING
<222> (1)..(8)
<223> /note="Putative GTP binding motif G1"

<400> 21
Ser Gly Ile Arg Leu Gly Ser Leu
1 5

<210> 22
<211> 8
<212> PRT
<213> Enterococcus faecalis

<220>
<221> BINDING
<222> (1)..(8)
<223> /note="Putative GTP binding motif G1"

<400> 22
Ala Gly Lys Arg Leu Gly Thr Ile
1 5

<210> 23
<211> 8
<212> PRT
<213> *Lactococcus lactis*

<220>
<221> BINDING
<222> (1)..(8)
<223> /note="Putative GTP binding motif G1"

<400> 23
Ser Gly Met Arg Leu Gly Thr Phe
1 5

<210> 24
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence GTP binding domain in CodY homologs

<220>
<221> Variant
<222> (2)..(2)
<223> Ala, Lys

<220>
<221> Variant
<222> (3)..(3)
<223> Phe, Ile

<400> 24
Asp Arg Val Gly
1

<210> 25
<211> 4
<212> PRT
<213> *Escherichia coli*

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G3"

<400> 25
Asp Ala Phe Gly
1

<210> 26
<211> 4

<212> PRT
<213> *Bacillus subtilis*

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G3"

<400> 26
Asp Arg Val Gly
1

<210> 27
<211> 4
<212> PRT
<213> *Clostridium difficile*

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G3"

<400> 27
Asp Arg Ile Gly
1

<210> 28
<211> 4
<212> PRT
<213> *Lactococcus lactis*

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G3"

<400> 28
Asp Lys Ile Gly
1

<210> 29
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence GTP motif in CodY homologs

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<220>

<221> VARIANT
<222> (3)..(3)
<223> Leu, Phe, Asn, Ser, Gln

<400> 29
Asn Lys Gly Asp
1

<210> 30
<211> 4
<212> PRT
<213> Escherichia coli

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 30
Thr Ser Leu Asp
1

<210> 31
<211> 4
<212> PRT
<213> Bacillus subtilis

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 31
Asn Lys Phe Leu
1

<210> 32
<211> 4
<212> PRT
<213> Bacillus stearothermophilus

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 32
Asp Lys Phe Leu
1

<210> 33
<211> 4
<212> PRT
<213> Clostridium difficile

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 33
Asn Glu Gly Ile
1

<210> 34
<211> 4
<212> PRT
<213> Clostridium acetobutylicum

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 34
Ile Leu Asn Asp
1

<210> 35
<211> 4
<212> PRT
<213> Streptococcus pneumoniae

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 35
Leu Ile Ser Asp
1

<210> 36
<211> 4
<212> PRT
<213> Enterococcus faecalis

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 36
Asn Gln Gln Phe

1

<210> 37
<211> 4
<212> PRT
<213> *Staphylococcus aureus*

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 37
Glu Lys Gly Ile
1

<210> 38
<211> 4
<212> PRT
<213> *Lactococcus lactis*

<220>
<221> BINDING
<222> (1)..(4)
<223> /note="Putative GTP binding motif G4"

<400> 38
Thr Gly Leu Phe
1

<210> 39
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in *yreE*

<400> 39
taatttctg ataatatagt caattt 26

<210> 40
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in *ctrA*

<400> 40
taatttactg acaagtctgt cagtaa 26

<210> 41
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in yciC

<400> 41
taatttactg acaaaaattat cagaac 26

<210> 42
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in optA

<400> 42
aaattttctg acaataataa aaatttg 26

<210> 43
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in optS

<400> 43
aaatttatcag aaaaatacaa caatat 26

<210> 44
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in optS

<400> 44
taattttcag aataatatga aaattc 26

<210> 45
<211> 26
<212> DNA

<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in parA

<400> 45
taatttactg atagatttgt cagtaa

26

<210> 46
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in aroF

<400> 46
taatttactg acagtttgt cagtaa

26

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in vacB1

<400> 47
aaatttactg acaaaaaaga taatgg

26

<210> 48
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in optA

<400> 48
taattttcag aaaacataac cattat

26

<210> 49
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in ypaG

<400> 49
gaatttatg aaaaaaatat taattg

26

<210> 50
<211> 26
<212> DNA

<213> Artificial Sequence

<220>

<223> presence of the putative CodY box in yiaB

<400> 50

gaatttactg acgaatctat cattaa

26

<210> 51

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> presence of the putative CodY box in ysdC

<400> 51

tcatctctcg acaaattctgt cagtaa

26

<210> 52

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> presence of the putative CodY box in hemK

<400> 52

aaatttactg acaagcttgt tagtat

26

<210> 53

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> presence of the putative CodY box in prfC

<400> 53

aaatttaatg ataaaacaat tagttt

26

<210> 54

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> presence of the putative CodY box in yugB

<400> 54

aaagttactg acaaattctgt cagtaa

26

<210> 55
<211> 26
<212> DNA
<213> Artificial Sequence.

<220>
<223> presence of the putative CodY box in murD

<400> 55
ttatTTactg acaagTctgt cagtaa 26

<210> 56
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in ywdG

<400> 56
tatTTTactg acaaaaaat aagttt 26

<210> 57
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in parC

<400> 57
taatTTactg acagctttgt cagtaa 26

<210> 58
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in pepC

<400> 58
aaatTTactg acagagctgt cagtaa 26

<210> 59
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in mutM

<400> 59

aaatttactg acagacttgt tagtaa

26

<210> 60
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in rgpAB

<400> 60
aaatttactg acaacttgt cagaag

26

<210> 61
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in vacB1

<400> 61
aaaatgtctg ataaaatgtat taatac

26

<210> 62
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in recN

<400> 62
taatttactg acagaatttt aaattt

26

<210> 63
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> presence of the putative CodY box in llrH

<400> 63
aaaattacta acaaaaactgt tagtaa

26

<210> 64
<211> 15
<212> DNA
<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 64

aattttcaga aaatt

15

<210> 65

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 65

aattgtcaga aaatt

15

<210> 66

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 66

aattttctga taatt

15

<210> 67

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 67

aattttcaga taatt

15

<210> 68

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 68

attttcaga aaatt

15

<210> 69

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 69

aattttcgga aaaat

15

<210> 70

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 70

aattttcaga aaata

15

<210> 71

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 71

acttttcaga aaatt

15

<210> 72

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 72

aattttctga atatt

15

<210> 73

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> motif in L. lactis MG1363 genome

<400> 73

atttttcaga aaaat

15

<210> 74
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> motif in L. lactis MG1363 genome

<400> 74
aattgtcaga caatt

15